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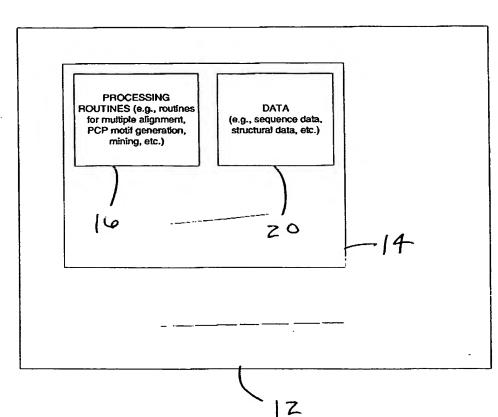
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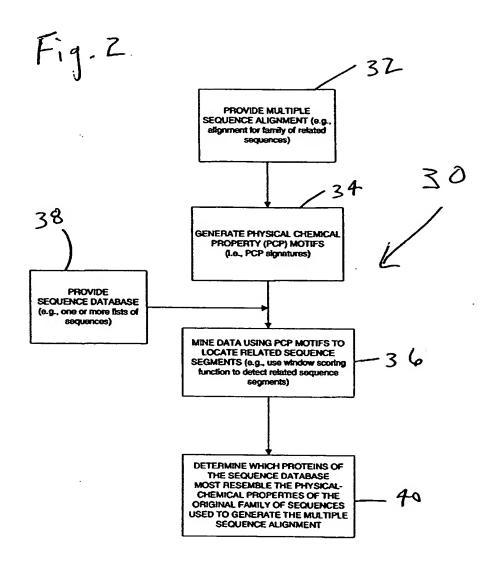
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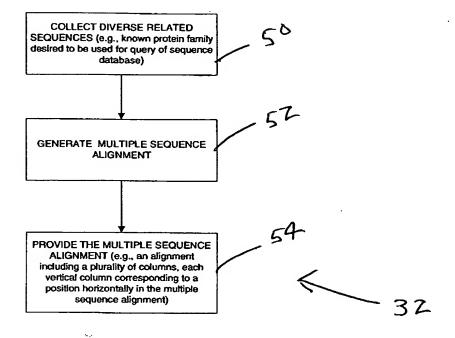


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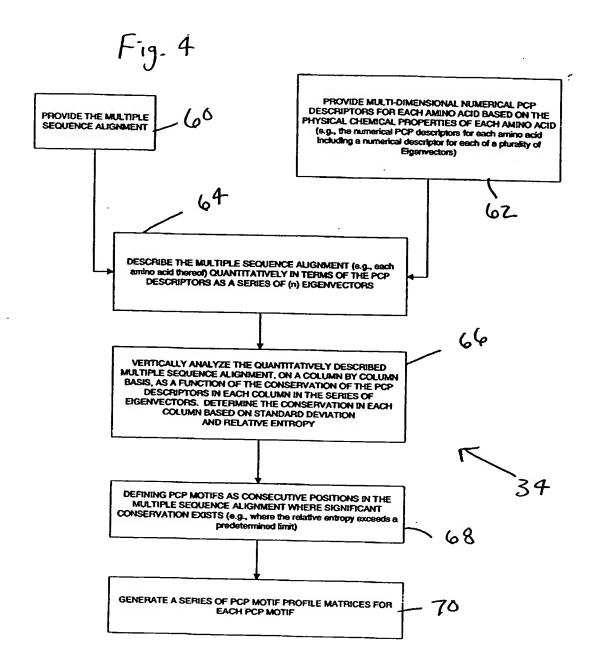
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Fig. 5 62 PROVIDE MULTI-DIMENSIONAL NUMERICAL PCP DESCRIPTORS FOR EACH AMINO ACID BASED ON THE PHYSICAL CHEMICAL PROPERTIES OF EACH AMINO ACID PROVIDE THE MULTIPLE SEQUENCE ALIGNMENT (e.g., the numerical PCP descriptors for each amino acid including a numerical descriptor for each of a plurality of Eigenvectors) DESCRIBE THE MULTIPLE SEQUENCE ALIGNMENT DESCRIBE THE MULTIFLE SEQUENCE ALIGNMENT QUANTITATIVELY IN TERMS OF THE PCP DESCRIPTORS RESULTING IN (N) DISTINCT PCP DESCRIBED AUGNMENTS CORRESPONDING TO THE N EIGENVECTORS, EACH DISTINCT ALIGNMENT INCLUDING COLUMNS CORRESPONDING TO THE COLUMNS (i.e., positions) OF THE MULTIPLE SEQUENCE ALIGNMENT, WHEREIN EACH COLUMN INCLUDES NUMERICAL 94 PCP DESCRIPTORS (i.e., corresponding to the eigenvector being defined) FOR EACH AMINO ACID (i.e., residue) IN THE COLUMN 86 ANALYZE EACH OF THE N PCP DESCRIBED ALIGNMENTS, COLUMN BY COLUMN, TO GENERATE CONSERVATION PROPERTY DATA FOR EACH COLUMN THEREOF (e.g., the conservation property data including the average value of each column and the related standard deviation for the column, and a relative entropy for the column) 34 88 SCANNING (e.g., horizontally across sequential columns that were analyzed) THE CONSERVATION PROPERTY DATA (e.g., the relative entropy values generated for each column of the PCP described 92 alignment being analyzed) TO DETECT CONSECUTIVE POSITIONS (e.g., corresponding to consecutively analyzed columns) WHERE THE RELATIVE ENTROPY EXCEEDS A PREDETERMINED LIMIT USER SPECIFIED GAP AND MINIMUM LENGTH LIMITS BASED ON THE DETECTED CONSECUTIVE POSITIONS AND USER SPECIFIED GAP AND MINIMUM LENGTH LIMITS, DETERMINING WHERE THE PCP MOTIFS ARE LOCATED IN THE MULTIPLE SEQUENCE ALIGNMENT 90 GENERATE A SERIES OF PCP MOTIF PROFILE MATRICES OR A MULTI-DIMENSIONAL MATRIX FOR EACH MOTIF (e.g., each motif defined by a plurality of matrices, with each matrix thereof corresponding to one of n eigenvectors, and further wherein each matrix includes a first level that includes average values for each

position in the PCP motif for the corresponding eigenvector and related standard deviation, and a second level that gives the relative entropy of each position of the PCP motif for the corresponding eigenvector)

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Fig. 6 102 PROVIDE SEQUENCE DATABASE TO BE SEARCHED (e.g., a plurality of proteins) PROVIDE THE PCP MOTIF PROFILE MATRICES USED TO DEFINE EACH PCP MOTIF CONVERT SEQUENCE DATABASE INTO SEARCHABLE FORM CORRESPONDING TO PCP MOTIF PROFILE MATRICES USING NUMERICAL PCP DESCRIPTORS (e.g., mon 104 matrices, where n is the number of Eigenvectors and m is the length of the sequence) MATCHING VALUES OF THE PCP MOTIF PROFILE
MATRICES TO WINDOWS OF THE SEQUENCES IN THE
CONVERTED SEQUENCE DATABASE USING A 186 POSITIONAL SCORING FUNCTION 108 SELECT ONE OR MORE SCORED WINDOWS AS BEING BEST MATCHES FOR THE PCP MOTIF PROFILE MATRICES USED TO DEFINE EACH PCP MOTIF PROVIDE FILE INCLUDING VALUES AND/OR SEQUENCES OF THE SEGMENTS OF SEARCHED SEQUENCES THAT ARE BEST MATCHED TO THE PCP MOTIF PROFILE MATRICES USED TO DEFINE EACH PCP MOTIF (e.g., matched areas of proteins PCP characteristics to the family used to generate the multiple sequence alignment but which have different amino acid sequences) 110

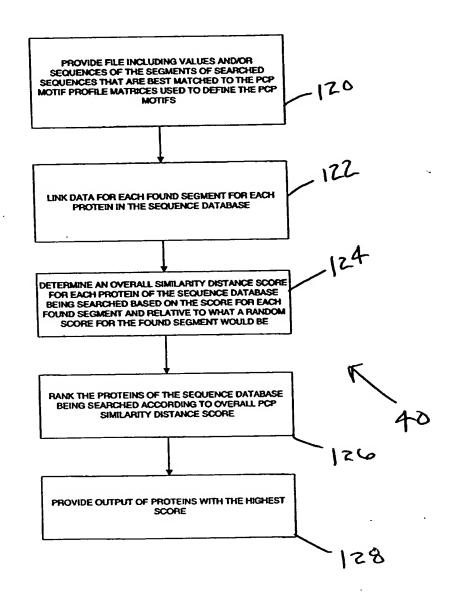
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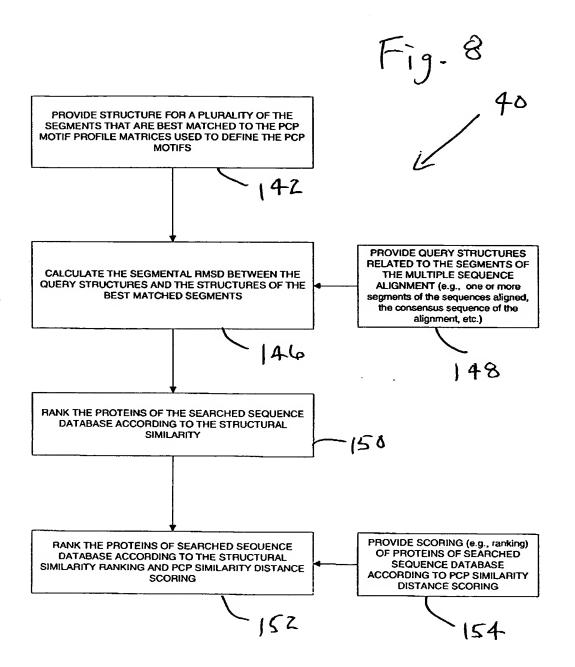
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וייסניו	_	(S1)	(S2)	(S3)	(S4)	(S4) 42 APE score	ASTRAL40
13	(DUMAN APE)					ave. ± std. dev	ave. ± std. dev
•	02 LAICS WN YDGLRA 74	0.91*	0.90*	0.63*	0.73*	$0.87 \pm 0.05$	0.56 ± 0.05
2	89 PDILCLQETK 98	0.96*	0.93*	0.84*	0.70*	$0.92 \pm 0.04$	$0.61 \pm 0.07$
w	125 KEGYSGVGLLSRQCP 139	0.91*	0.86*	0.60	0 20 20 20 20 20 20 20 20 20 20 20 20 20	0 85 + 0 05	064 + 0.07
_				0.00	3	0.65 + 0.00	C.04 I U.U3
1	143 GIGDEEHDQEGRVIVAEFDSFVL 169 0.94*	0.94*	0.77*	0.71	0.81	$0.84 \pm 0.09$	0.67 + 0.07
S	171 YVPNA 175	0.96*	0.96*	0.68	> 8 8	001+006	0.60 ± 0.07
<b>X</b>		0				C. 77 H C. CC	0.00 I 0.10
2 (		0.80*	0.70*	0.78	0.77	$0.74 \pm 0.06$	$0.67 \pm 0.05$
7	204 PLVLCGDLNVAH 215	0.96*	0.88*	0.82*	0.78*	$0.90 \pm 0.04$	$0.55 \pm 0.08$
œ	231 GFTPQERQGFGEL 243	0.96*	0.91*	0.78	0.73	$0.87 \pm 0.09$	0 70 + 0 07
9	247 VPLADSFR 254	000		3			
5		0.70	0.95	2	0.00	0.91 ± 0.08	$0.74 \pm 0.11$
E	264 YTFWTYM 270	0.86*	0.77*	0.61	0.70	$0.84 \pm 0.08$	$0.61 \pm 0.06$
Ξ	274 RSKNVGWRLDYFLLSHSL 291	0.92*	0.89*	0.56	<u>2</u>	$0.90 \pm 0.04$	0 54 + 0 07
12	306 GSDHCPI 312	0.93*	0.94*	0.88*	0.83*	0.83* 0.92 ± 0.03	0.52 + 0.09

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PDB'	Score in bits (fraction to	Motifs found	SCOP <sup>3</sup>	EC	Description
	the highest score)				
IHD7	1942 (1.00)	1.2.3.4.5.6.7.8.9.10.11.12	1 1 1 P	4 3 00 19	A 3.7
1AKO	1861 (0.06)	1,4,5,7,5,0,7,10,11,12	0.151.1.1	4.2.99.18	APE
מלכי ל	1007 (0.30)	1,2,3,4,5,7,8,9,10,11,12	d.151.1.1	3.1.11.2	Exonuclease III
CN7	1094 (0.56)	2,6,7,12	d.151.1.1	0.0.0.0	Denyvrihonnolesse I
1194	1056 (0.54)	1,4,5,6,7,9,12	d 151 1.2	0000	Phonbatishiling it   1   1   2
1 <b>B</b> 3U	840 (0.43)	5.7.9.12	9 118 1 2	0.000	Position of phosphate synaptic
IMDA	814 (0.42)	6.9.11.12	7 80 3 1	1 4 00 3	weguatory domain or protein phospi
MPY	707 (0.41)			L. 77.1	viculy amine denydrogenase
אמטו	700 (0.12)		L.1.2C.1	1.13.11.2	Catechol 2,3-dioxygenase
IN COLVE	/92 (0.41)		<b>b.30.2.1</b>	1.4.3.6	Copper amine oxidase
IXKG	737 (0.38)	2,9,12	c.10.1.2	0.0.0	Omese BNA 1
1009	698 (0.36)		c.56.5.4	3411	A minopentidate
PDB ∞d	PDB code of the protein				Aminopopulase
SCOP ∞	de and d.151.1 is	<sup>2</sup> SCOP code and d.151.1 is the DNasel superfamily code	de		
Pnzyme /	Darring commission of the second				

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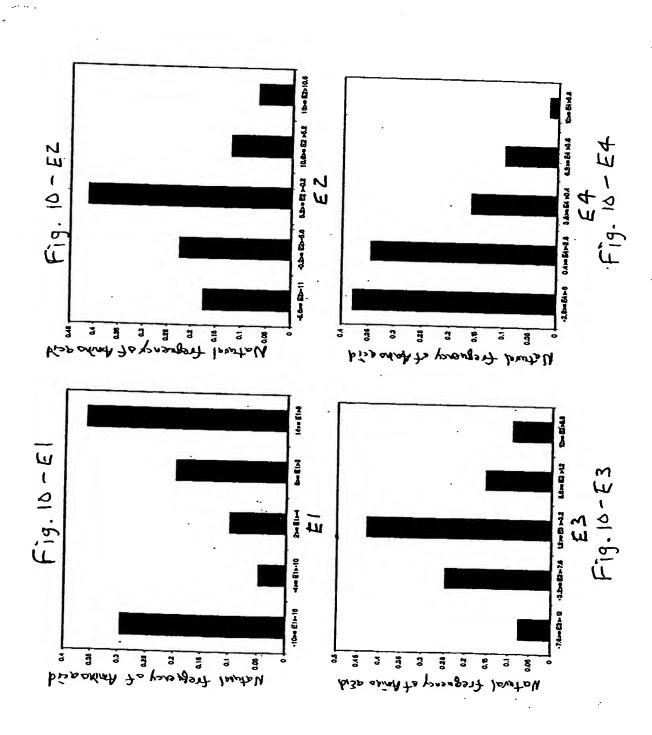
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PDB.	Score in bits (fraction to the highest	MOLEGOS found	SCOP.	БĊ	Description
1477	score)	1334573655			
IAKO	1942 (1.00)	1,2,3,4,5,6,7,8,9,10,11,12	d.151.1.1	4.2.99.18	APE (Mn/Mg/Pb)
	1831 (0.94)	1,2,3,5,6,7,8,9,10,11,12	d.151.1.1	3.1.11.2	Exonuclease III
2DNJ	1072 (0.55)	1,2,5,6,7,9,10,12	d 151 1	2 - 21 -	Daniel Services III
Y611	971 (0.50)	1.2.5.6.7.9.10.12	7 171 J	3.1.2.1.1	Deoxymbonuclease I
Į Q	698 (0.36)	5.6.9.10.12	0.56.5.4	2 / 1	r nospitatioyimositoi phosphate Synaptojanii
IATL	633 (0.33)	5,6,9,10,12	d 92 1 9	3 4 3 4 4 4 5	Aminopephoase (Zn, Ca)
1D09	619 (0.32)	5.9.12	7 00 7	0100	onake venom metalloprotease (Zn, Ca)
ID2N	613 (0.32)	5.6.8.9.12	27 1 12	4.1.3.4	Aspartate caroamoyitransferase (Zn)
IDOB .	579 (0.30)	2,5,9,12	c.10.2.1		Internal in the second of sensitive fusion prote
1 EEM	571 (0.29)	5,6,8,12	a.45.1.1		Chitathian C track domain (Ca)
PDB ∞d	PDB code of the protein				Citiannoite 3-transierase
SCOP co	de and d.151.1 is	<sup>2</sup> SCOP code and d.151.1 is the DNasel superfamily code	<del>d</del> e		
Enzyme c	<sup>1</sup> Enzyme commission classification number	ification number			

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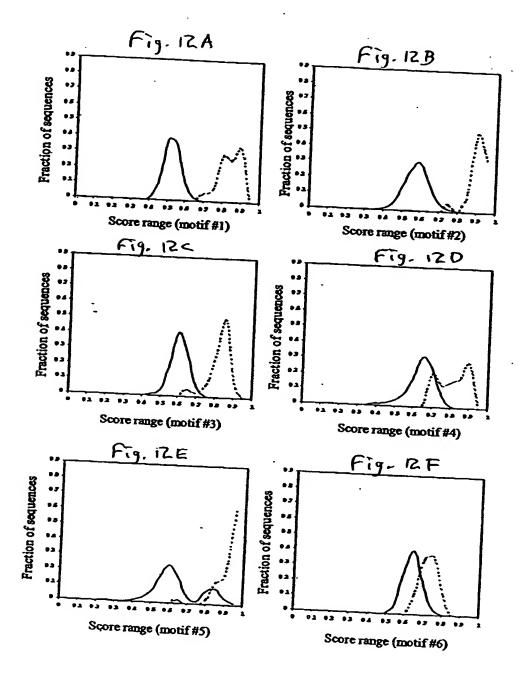
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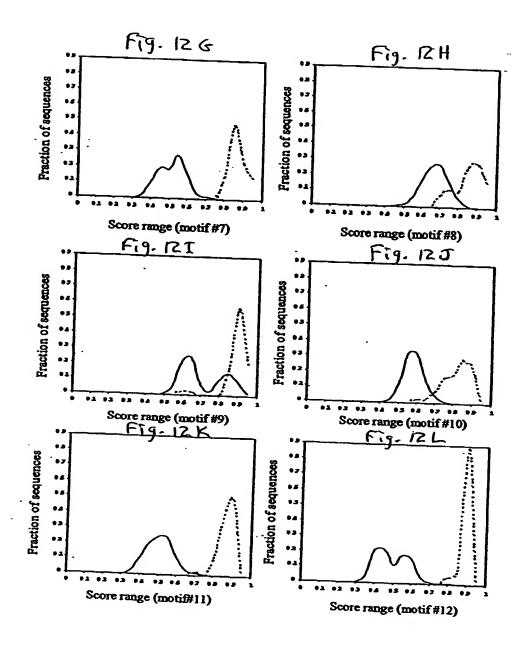
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Fig. 14

